	GIII	101		i nis	arg	ser	101		. vaı	. lie	Pro	102	_	Glu	Ala	Glu
5	Val 102		Gln	Glu	Val	Arg 103		Cys	Pro	Gly	Arg	_	Tyr	Ile	Leu	Arg 1040
10	Val	Thr	Ala	Tyr	Lys 104		Gly	Tyr	Gly	Glu 105	_	Cys	Val	Thr	Ile 105	
	Glu	Ile	Glu	Asp 106		Thr	Asp	Glu	Leu 106	Lys 5	Phe	Ser	Asn	Cys		Glu
15	Glu	Glu	Val 107		Pro	Asn	Asn	Thr		Thr	Cys	Asn	Asn 108!	-	Thr	Gly
	Thr	Gln 109		Glu	Tyr	Glu	Gly 109		Tyr	Thr	Ser	Arg		Gln	Gly	Tyr
20 	Asp 1105		Ala	Tyr	Gly	Asn 1110		Pro	Ser	Val	Pro 1115		Asp	Tyr	Ala	Ser 1120
] 25	Val	Tyr	Glu	Glu	Lys 1125		Tyr	Thr	Asp	Gly 1130		Arg	Glu	Asn	Pro 1135	-
22 120000000000000000000000000000000000	Glu	Ser	Asn	Arg 1140		Tyr	Gly	Asp	Tyr 1145	Thr	Pro	Leu	Pro	Ala 1150		Tyr
3 0	Val	Thr	Lys 1155		Leu	Glu	Tyr	Phe 1160		Glu	Thr	Asp	Lys 1165		Trp	Ile
	Glu	Ile 1170		Glu	Thr	Glu	Gly 1175		Phe	Ile	Val	Asp 1180		Val	Glu	Leu
<u>3</u> 5	Leu 1185		Met	Glu	Glu											
40	(2)		RMAT			_										
		(i)		L) LE	ENGTH	IARAC I: 35 nucl	67 b	ase	pair	îs						
45						EDNE GY:		_	rle							
50		(ix)		A) NA	ME/F	ŒY:		3567								
50		(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	ON: 9	EQ I	D NC):5:					

	Glu		Gln			Pro			AGT Ser		48
5	CCT Pro										96
10	TCA Ser									1	144
15	GTA Val 50									1	.92
20	ATA Ile									2	40
2000 2000 2000 2000 2000 2000 2000 200	TTA Leu									2	88
25	AAT Asn									3:	36
30	AAA Lys									31	84
	ATT Ile 130									4 :	32
40	TCG Ser									4	80
	C AA Gln	•								5	28
45	GGA Gly									5	76
50	AGA Arg									6	24

		Asn						Thr		GAT Asp	672
5	Ile	ACA Thr								TTA Leu 240	720
10		GCC Ala									768
15		GTT Val									816
20		AAT Asn 275									864
20 10 10 25 25		GAG Glu		 					 		912
25		CTT Leu									960
3 0 3 0 3 0 3 0 3 0 3 0 3 0 3 0 3 0 3 0		GGA Gly									1008
35		TCT Ser									1056
40		ACT Thr 355									1104
40	 	TTA Leu	-	 	 						1152
45		GAA Glu									1200
50		AGA Arg									1248